

SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT: Gray, Patrick W.
- (ii) TITLE OF INVENTION: Chitinase Materials and Methods
- (iii) NUMBER OF SEQUENCES: 15
- (iv) CORRESPONDENCE ADDRESS:
 - (A) ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
 - (B) STREET: 6300 Sears Tower, 233 South Wacker Drive
 - (C) CITY: Chicago
 - (D) STATE: Illinois
 - (E) COUNTRY: United States of America
 - (F) ZIP: 60606-6402
- (v) COMPUTER READABLE FORM:
 - (A) MEDIUM TYPE: Floppy disk
 - (B) COMPUTER: IBM PC compatible
 - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
 - (D) SOFTWARE: PatentIn Release #1.0, Version #1.25
- (vi) CURRENT APPLICATION DATA:
 - (A) APPLICATION NUMBER:
 - (B) FILING DATE:
 - (C) CLASSIFICATION:
- (viii) ATTORNEY/AGENT INFORMATION:
 - (A) NAME: Rin-Laures, Li-Hsien
 - (B) REGISTRATION NUMBER: 33,547
 - (C) REFERENCE/DOCKET NUMBER: 27866/32960
- (ix) TELECOMMUNICATION INFORMATION:
 - (A) TELEPHONE: 312/474-6300
 - (B) TELEFAX: 312/474-0448
 - (C) TELEX: 25-3856

(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1636 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (ix) FEATURE:
 - (A) NAME/KEY: CDS
 - (B) LOCATION: 2..1399
- (ix) FEATURE:
 - (A) NAME/KEY: mat_peptide
 - (B) LOCATION: 65..1399
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

C	ATG	GTG	CGG	TCT	GTG	GCC	TGG	GCA	GGT	TTC	ATG	GTC	CTG	CTG	ATG	46
	Met	Val	Arg	Ser	Val	Ala	Trp	Ala	Gly	Phe	Met	Val	Leu	Leu	Met	
	-21	-20					-15						-10			
ATC	CCA	TGG	GGC	TCT	GCT	GCA	AAA	CTG	GTC	TGC	TAC	TTC	ACC	AAC	TGG	94

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Ile	Pro	Trp	Gly	Ser	Ala	Ala	Lys	Leu	Val	Cys	Tyr	Phe	Thr	Asn	Trp		
	-5					1				5					10		
GCC	CAG	TAC	AGA	CAG	GGG	GAG	GCT	CGC	TTC	CTG	CCC	AAG	GAC	TTG	GAC	142	
Ala	Gln	Tyr	Arg	Gln	Gly	Glu	Ala	Arg	Phe	Leu	Pro	Lys	Asp	Leu	Asp	25	
				15				20									
CCC	AGC	CTT	TGC	ACC	CAC	CTC	ATC	TAC	GCC	TTC	GCT	GGC	ATG	ACC	AAC	190	
Pro	Ser	Leu	Cys	Thr	His	Leu	Ile	Tyr	Ala	Phe	Ala	Gly	Met	Thr	Asn	40	
			30					35									
CAC	CAG	CTG	AGC	ACC	ACT	GAG	TGG	AAT	GAC	GAG	ACT	CTC	TAC	CAG	GAG	238	
His	Gln		Leu	Ser	Thr	Thr	Glu	Trp	Asn	Asp	Glu	Thr	Leu	Tyr	Gln	Glu	
			45					50					55				
TTC	AAT	GGC	CTG	AAG	AAG	ATG	AAT	CCC	AAG	CTG	AAG	ACC	CTG	TTA	GCC	286	
Phe	Asn	Gly	Leu	Lys	Lys	Met	Asn	Pro	Lys	Leu	Lys	Thr	Leu	Leu	Ala		
	60					65						70					
ATC	GGA	GGC	TGG	AAT	TTC	GGC	ACT	CAG	AAG	TTC	ACA	GAT	ATG	GTA	GCC	334	
Ile	Gly	Gly	Trp	Asn	Phe	Gly	Thr	Gln	Lys	Phe	Thr	Asp	Met	Val	Ala	90	
	75				80					85							
ACG	GCC	AAC	AAC	CGT	CAG	ACC	TTT	GTC	AAC	TCG	GCC	ATC	AGG	TTT	CTG	382	
Thr	Ala	Asn	Asn	Arg	Gln	Thr	Phe	Val	Asn	Ser	Ala	Ile	Arg	Phe	Leu	105	
				95					100								
CGC	AAA	TAC	AGC	TTT	GAC	GGC	CTT	GAC	CTT	GAC	TGG	GAG	TAC	CCA	GGA	430	
Arg	Lys	Tyr	Ser	Phe	Asp	Gly	Leu	Asp	Leu	Asp	Trp	Glu	Tyr	Pro	Gly	120	
				110				115									
AGC	CAG	GGG	AGC	CCT	GCC	GTA	GAC	AAG	GAG	CGC	TTC	ACA	ACC	CTG	GTA	478	
Ser	Gln	Gly	Ser	Pro	Ala	Val	Asp	Lys	Glu	Arg	Phe	Thr	Thr	Leu	Val		
				125			130					135					
CAG	GAC	TTG	GCC	AAT	GCC	TTC	CAG	CAG	GAA	GCC	CAG	ACC	TCA	GGG	AAG	526	
Gln	Asp	Leu	Ala	Asn	Ala	Phe	Gln	Gln	Glu	Ala	Gln	Thr	Ser	Gly	Lys		
	140					145						150					
GAA	CGC	CTT	CTT	CTG	AGT	GCA	GCG	GTT	CCA	GCT	GGG	CAG	ACC	TAT	GTG	574	
Glu	Arg	Leu	Leu	Leu	Ser	Ala	Ala	Val	Pro	Ala	Gly	Gln	Thr	Tyr	Val	170	
	155				160					165							
GAT	GCT	GGA	TAC	GAG	GTG	GAC	AAA	ATC	GCC	CAG	AAC	CTG	GAT	TTT	GTC	622	
Asp	Ala	Gly	Tyr	Glu	Val	Asp	Lys	Ile	Ala	Gln	Asn	Leu	Asp	Phe	Val	185	
				175					180								
AAC	CTT	ATG	GCC	TAC	GAC	TTC	CAT	GGC	TCT	TGG	GAG	AAG	GTC	ACG	GGA	670	
Asn	Leu	Met	Ala	Tyr	Asp	Phe	His	Gly	Ser	Trp	Glu	Lys	Val	Thr	Gly	200	
				190				195									
CAT	AAC	AGC	CCC	CTC	TAC	AAG	AGG	CAA	GAA	GAG	AGT	GGT	GCA	GCA	GCC	718	
His	Asn	Ser	Pro	Leu	Tyr	Lys	Arg	Gln	Glu	Glu	Ser	Gly	Ala	Ala	Ala	215	
				205			210										
AGC	CTC	AAC	GTG	GAT	GCT	GCT	GTG	CAA	CAG	TGG	CTG	CAG	AAG	GGG	ACC	766	
Ser	Leu	Asn	Val	Asp	Ala	Ala	Val	Gln	Gln	Trp	Leu	Gln	Lys	Gly	Thr		
				220			225					230					
CCT	GCC	AGC	AAG	CTG	ATC	CTT	GGC	ATG	CCT	ACC	TAC	GGA	CGC	TCC	TTC	814	
Pro	Ala	Ser	Lys	Leu	Ile	Leu	Gly	Met	Pro	Thr	Tyr	Gly	Arg	Ser	Phe	250	
					240					245							
ACA	CTG	GCC	TCC	TCA	TCA	GAC	ACC	AGA	GTG	GGG	GCC	CCA	GCC	ACA	GGG	862	
Thr	Leu	Ala	Ser	Ser	Ser	Asp	Thr	Arg	Val	Gly	Ala	Pro	Ala	Thr	Gly		

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				255					260					265			
TCT	GGC	ACT	CCA	GGC	CCC	TTC	ACC	AAG	GAA	GGA	GGG	ATG	CTG	GCC	TAC		910
Ser	Gly	Thr	Pro	Gly	Pro	Phe	Thr	Lys	Glu	Gly	Gly	Met	Leu	Ala	Tyr		
			270					275					280				
TAT	GAA	GTC	TGC	TCC	TGG	AAG	GGG	GCC	ACC	AAA	CAG	AGA	ATC	CAG	GAT		958
Tyr	Glu	Val	Cys	Ser	Trp	Lys	Gly	Ala	Thr	Lys	Gln	Arg	Ile	Gln	Asp		
		285				290					295						
CAG	AAG	GTG	CCC	TAC	ATC	TTC	CGG	GAC	AAC	CAG	TGG	GTG	GGC	TTT	GAT		1006
Gln	Lys	Val	Pro	Tyr	Ile		Arg	Asp	Asn	Gln	Trp	Val	Gly	Phe	Asp		
	300				305						310						
GAT	GTG	GAG	AGC	TTC	AAA	ACC	AAG	GTC	AGC	TAT	CTG	AAG	CAG	AAG	GGA		1054
Asp	Val	Glu	Ser	Phe	Lys	Thr	Lys	Val	Ser	Tyr	Leu	Lys	Gln	Lys	Gly		
	315				320					325					330		
CTG	GGC	GGG	GCC	ATG	GTC	TGG	GCA	CTG	GAC	TTA	GAT	GAC	TTT	GCC	GGC		1102
Leu	Gly	Gly	Ala	Met	Val	Trp	Ala	Leu	Asp	Leu	Asp	Asp	Phe	Ala	Gly		
			335						340					345			
TTC	TCC	TGC	AAC	CAG	GGC	CGA	TAC	CCC	CTC	ATC	CAG	ACG	CTA	CGG	CAG		1150
Phe	Ser	Cys	Asn	Gln	Gly	Arg	Tyr	Pro	Leu	Ile	Gln	Thr	Leu	Arg	Gln		
			350					355					360				
GAA	CTG	AGT	CTT	CCA	TAC	TTG	CCT	TCA	GGC	ACC	CCA	GAG	CTT	GAA	GTT		1198
Glu	Leu	Ser	Leu	Pro	Tyr	Leu	Pro	Ser	Gly	Thr	Pro	Glu	Leu	Glu	Val		
		365				370					375						
CCA	AAA	CCA	GGT	CAG	CCC	TCT	GAA	CCT	GAG	CAT	GGC	CCC	AGC	CCT	GGA		1246
Pro	Lys	Pro	Gly	Gln	Pro	Ser	Glu	Pro	Glu	His	Gly	Pro	Ser	Pro	Gly		
	380				385						390						
CAA	GAC	ACG	TTC	TGC	CAG	GGC	AAA	GCT	GAT	GGG	CTC	TAT	CCC	AAT	CCT		1294
Gln	Asp	Thr	Phe	Cys	Gln	Gly	Lys	Ala	Asp	Gly	Leu	Tyr	Pro	Asn	Pro		
	395				400					405					410		
CGG	GAA	CGG	TCC	AGC	TTC	TAC	AGC	TGT	GCA	GCG	GGG	CGG	CTG	TTC	CAG		1342
Arg	Glu	Arg	Ser	Ser	Phe	Tyr	Ser	Cys	Ala	Ala	Gly	Arg	Leu	Phe	Gln		
			415					420					425				
CAA	AGC	TGC	CCG	ACA	GGC	CTG	GTG	TTC	AGC	AAC	TCC	TGC	AAA	TGC	TGC		1390
Gln	Ser	Cys	Pro	Thr	Gly	Leu	Val	Phe	Ser	Asn	Ser	Cys	Lys	Cys	Cys		
			430				435						440				
ACC	TGG	AAT	TGAGTCGCTA	AAGCCCCTCC	AGTCCCAGCT	TTGAGGCTGG											1439
Thr	Trp	Asn															
		445															
GCCCAGGATC	ACTCTACAGC	CTGCCTCCTG	GGTTTTCCT	GGGGGCCGCA	ATCTGGCTCC												1499
TGCAGGCCCTT	TCTGTGGTCT	TCCTTTATCC	AGGCTTCTG	CTCTCAGCCT	TGCCTTCCTT												1559
TTTTCTGGGT	CTCCTGGGCT	GCCCTTTTCA	CTTGCAAAAT	AAATCTTTGG	TTTGTGCCCC												1619
TCTTCCCAAA	AAAAAAA																1636

(2) INFORMATION FOR SEQ ID NO:2:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 466 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

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(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met Val Arg Ser Val Ala Trp Ala Gly Phe Met Val Leu Leu Met Ile
-21 -20 -15 -10
Pro Trp Gly Ser Ala Ala Lys Leu Val Cys Tyr Phe Thr Asn Trp Ala
-5 1 5 10
Gln Tyr Arg Gln Gly Glu Ala Arg Phe Leu Pro Lys Asp Leu Asp Pro
15 20 25
Ser Leu Cys Thr His Leu Ile Tyr Ala Phe Ala Gly Met Thr Asn His
30 35 40
Gln Leu Ser Thr Thr Glu Trp Asn Asp Glu Thr Leu Tyr Gln Glu Phe
45 50 55
Asn Gly Leu Lys Lys Met Asn Pro Lys Leu Lys Thr Leu Leu Ala Ile
60 65 70 75
Gly Gly Trp Asn Phe Gly Thr Gln Lys Phe Thr Asp Met Val Ala Thr
80 85 90
Ala Asn Asn Arg Gln Thr Phe Val Asn Ser Ala Ile Arg Phe Leu Arg
95 100 105
Lys Tyr Ser Phe Asp Gly Leu Asp Leu Asp Trp Glu Tyr Pro Gly Ser
110 115 120
Gln Gly Ser Pro Ala Val Asp Lys Glu Arg Phe Thr Thr Leu Val Gln
125 130 135
Asp Leu Ala Asn Ala Phe Gln Gln Glu Ala Gln Thr Ser Gly Lys Glu
140 145 150 155
Arg Leu Leu Leu Ser Ala Ala Val Pro Ala Gly Gln Thr Tyr Val Asp
160 165 170
Ala Gly Tyr Glu Val Asp Lys Ile Ala Gln Asn Leu Asp Phe Val Asn
175 180 185
Leu Met Ala Tyr Asp Phe His Gly Ser Trp Glu Lys Val Thr Gly His
190 195 200
Asn Ser Pro Leu Tyr Lys Arg Gln Glu Glu Ser Gly Ala Ala Ala Ser
205 210 215
Leu Asn Val Asp Ala Ala Val Gln Gln Trp Leu Gln Lys Gly Thr Pro
220 225 230 235
Ala Ser Lys Leu Ile Leu Gly Met Pro Thr Tyr Gly Arg Ser Phe Thr
240 245 250
Leu Ala Ser Ser Ser Asp Thr Arg Val Gly Ala Pro Ala Thr Gly Ser
255 260 265
Gly Thr Pro Gly Pro Phe Thr Lys Glu Gly Gly Met Leu Ala Tyr Tyr
270 275 280
Glu Val Cys Ser Trp Lys Gly Ala Thr Lys Gln Arg Ile Gln Asp Gln
285 290 295
Lys Val Pro Tyr Ile Phe Arg Asp Asn Gln Trp Val Gly Phe Asp Asp

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300 305 310 315
Val Glu Ser Phe Lys Thr Lys Val Ser Tyr Leu Lys Gln Lys Gly Leu
320 325 330
Gly Gly Ala Met Val Trp Ala Leu Asp Leu Asp Asp Phe Ala Gly Phe
335 340 345
Ser Cys Asn Gln Gly Arg Tyr Pro Leu Ile Gln Thr Leu Arg Gln Glu
350 355 360
Leu Ser Leu Pro Tyr Leu Pro Ser Gly Thr Pro Glu Leu Glu Val Pro
365 370 375
Lys Pro Gly Gln Pro Ser Glu Pro Glu His Gly Pro Ser Pro Gly Gln
380 385 390 395
Asp Thr Phe Cys Gln Gly Lys Ala Asp Gly Leu Tyr Pro Asn Pro Arg
400 405 410
Glu Arg Ser Ser Phe Tyr Ser Cys Ala Ala Gly Arg Leu Phe Gln Gln
415 420 425
Ser Cys Pro Thr Gly Leu Val Phe Ser Asn Ser Cys Lys Cys Cys Thr
430 435 440
Trp Asn
445

(2) INFORMATION FOR SEQ ID NO:3:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1656 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

- (ix) FEATURE:
(A) NAME/KEY: CDS
(B) LOCATION: 27..1424

- (ix) FEATURE:
(A) NAME/KEY: mat_peptide
(B) LOCATION: 90..1424

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

GCTGCAGCCT GCCGCTGAGC TGCATC ATG GTG CGG TCT GTG GCC TGG GCA GGT 53
Met Val Arg Ser Val Ala Trp Ala Gly
-21 -20 -15
TTC ATG GTC CTG CTG ATG ATC CCA TGG GGC TCT GCT GCA AAA CTG GTC 101
Phe Met Val Leu Leu Met Ile Pro Trp Gly Ser Ala Ala Lys Leu Val
-10 -5 1
TGC TAC TTC ACC AAC TGG GCC CAG TAC AGA CAG GGG GAG GCT CGC TTC 149
Cys Tyr Phe Thr Asn Trp Ala Gln Tyr Arg Gln Gly Glu Ala Arg Phe
5 10 15 20
CTG CCC AAG GAC TTG GAC CCC AGC CTT TGC ACC CAC CTC ATC TAC GCC 197
Leu Pro Lys Asp Leu Asp Pro Ser Leu Cys Thr His Leu Ile Tyr Ala
25 30 35

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TTC GCT GGC ATG ACC AAC CAC CAG CTG AGC ACC ACT GAG TGG AAT GAC	245
Phe Ala Gly Met Thr Asn His Gln Leu Ser Thr Thr Glu Trp Asn Asp	
40 45 50	
GAG ACT CTC TAC CAG GAG TTC AAT GGC CTG AAG AAG ATG AAT CCC AAG	293
Glu Thr Leu Tyr Gln Glu Phe Asn Gly Leu Lys Lys Met Asn Pro Lys	
55 60 65	
CTG AAG ACC CTG TTA GCC ATC GGA GGC TGG AAT TTC AGC ACT CAG AAG	341
Leu Lys Thr Leu Leu Ala Ile Gly Gly Trp Asn Phe Ser Thr Gln Lys	
70 75 80	
TTC ACA GAT ATG GTA GCC ACG GCC AAC AAC CGT CAG ACC TTT GTC AAC	389
Phe Thr Asp Met Val Ala Thr Ala Asn Asn Arg Gln Thr Phe Val Asn	
85 90 95 100	
TCG GCC ATC AGG TTT CTG CGC AAA TAC AGC TTT GAC GGC CTT GAC CTT	437
Ser Ala Ile Arg Phe Leu Arg Lys Tyr Ser Phe Asp Gly Leu Asp Leu	
105 110 115	
GAC TGG GAG TAC CCA GGA AGC CAG GGG AGC CCT GCC GTA GAC AAG GAG	485
Asp Trp Glu Tyr Pro Gly Ser Gln Gly Ser Pro Ala Val Asp Lys Glu	
120 125 130	
CGC TTC ACA ACC CTG GTA CAG GAC TTG GCC AAT GCC TTC CAG CAG GAA	533
Arg Phe Thr Thr Leu Val Gln Asp Leu Ala Asn Ala Phe Gln Gln Glu	
135 140 145	
GCC CAG ACC TCA GGG AAG GAA CGC CTT CTT CTG AGT GCA GCG GTT CCA	581
Ala Gln Thr Ser Gly Lys Glu Arg Leu Leu Leu Ser Ala Ala Val Pro	
150 155 160	
GCT GGG CAG ACC TAT GTG GAT GCT GGA TAC GAG GTG GAC AAA ATC GCC	629
Ala Gly Gln Thr Tyr Val Asp Ala Gly Tyr Glu Val Asp Lys Ile Ala	
165 170 175 180	
CAG AAC CTG GAT TTT GTC AAC CTT ATG GCC TAC GAC TTC CAT GGC TCT	677
Gln Asn Leu Asp Phe Val Asn Leu Met Ala Tyr Asp Phe His Gly Ser	
185 190 195	
TGG GAG AAG GTC ACG GGA CAT AAC AGC CCC CTC TAC AAG AGG CAA GAA	725
Trp Glu Lys Val Thr Gly His Asn Ser Pro Leu Tyr Lys Arg Gln Glu	
200 205 210	
GAG AGT GGT GCA GCA GCC AGC CTC AAC GTG GAT GCT GCT GTG CAA CAG	773
Glu Ser Gly Ala Ala Ala Ser Leu Asn Val Asp Ala Ala Val Gln Gln	
215 220 225	
TGG CTG CAG AAG GGG ACC CCT GCC AGC AAG CTG ATC CTT GGC ATG CCT	821
Trp Leu Gln Lys Gly Thr Pro Ala Ser Lys Leu Ile Leu Gly Met Pro	
230 235 240	
ACC TAC GGA CGC TCC TTC ACA CTG GCC TCC TCA TCA GAC ACC AGA GTG	869
Thr Tyr Gly Arg Ser Phe Thr Leu Ala Ser Ser Ser Asp Thr Arg Val	
245 250 255 260	
GGG GCC CCA GCC ACA GGG TCT GGC ACT CCA GGC CCC TTC ACC AAG GAA	917
Gly Ala Pro Ala Thr Gly Ser Gly Thr Pro Gly Pro Phe Thr Lys Glu	
265 270 275	
GGA GGG ATG CTG GCC TAC TAT GAA GTC TGC TCC TGG AAG GGG GCC ACC	965
Gly Gly Met Leu Ala Tyr Tyr Glu Val Cys Ser Trp Lys Gly Ala Thr	
280 285 290	
AAA CAG AGA ATC CAG GAT CAG AAG GTG CCC TAC ATC TTC CGG GAC AAC	1013

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Lys	Gln	Arg	Ile	Gln	Asp	Gln	Lys	Val	Pro	Tyr	Ile	Phe	Arg	Asp	Asn	
		295					300					305				
CAG	TGG	GTG	GGC	TTT	GAT	GAT	GTG	GAG	AGC	TTC	AAA	ACC	AAG	GTC	AGC	1061
Gln	Trp	Val	Gly	Phe	Asp	Asp	Val	Glu	Ser	Phe	Lys	Thr	Lys	Val	Ser	
	310					315					320					
TAT	CTG	AAG	CAG	AAG	GGA	CTG	GGC	GGG	GCC	ATG	GTC	TGG	GCA	CTG	GAC	1109
Tyr	Leu	Lys	Gln	Lys	Gly	Leu	Gly	Gly	Ala	Met	Val	Trp	Ala	Leu	Asp	
	325				330					335					340	
TTA	GAT	GAC	TTT	GCC	GGC	TTC	TCC	TGC	AAC	CAG	GGC	CGA	TAC	CCC	CTC	1157
Leu	Asp	Asp	Phe	Ala	Gly	Phe	Ser	Cys	Asn	Gln	Gly	Arg	Tyr	Pro	Leu	
				345					350					355		
ATC	CAG	ACG	CTA	CGG	CAG	GAA	CTG	AGT	CTT	CCA	TAC	TTG	CCT	TCA	GGC	1205
Ile	Gln	Thr	Leu	Arg	Gln	Glu	Leu	Ser	Leu	Pro	Tyr	Leu	Pro	Ser	Gly	
			360				365						370			
ACC	CCA	GAG	CTT	GAA	GTT	CCA	AAA	CCA	GGT	CAG	CCC	TCT	GAA	CCT	GAG	1253
Thr	Pro	Glu	Leu	Glu	Val	Pro	Lys	Pro	Gly	Gln	Pro	Ser	Glu	Pro	Glu	
		375				380					385					
CAT	GGC	CCC	AGC	CCT	GGA	CAA	GAC	ACG	TTC	TGC	CAG	GGC	AAA	GCT	GAT	1301
His	Gly	Pro	Ser	Pro	Gly	Gln	Asp	Thr	Phe	Cys	Gln	Gly	Lys	Ala	Asp	
	390					395					400					
GGG	CTC	TAT	CCC	AAT	CCT	CGG	GAA	CGG	TCC	AGC	TTC	TAC	AGC	TGT	GCA	1349
Gly	Leu	Tyr	Pro	Asn	Pro	Arg	Glu	Arg	Ser	Ser	Phe	Tyr	Ser	Cys	Ala	
	405				410					415					420	
GCG	GGG	CGG	CTG	TTC	CAG	CAA	AGC	TGC	CCG	ACA	GGC	CTG	GTG	TTC	AGC	1397
Ala	Gly	Arg	Leu	Phe	Gln	Gln	Ser	Cys	Pro	Thr	Gly	Leu	Val	Phe	Ser	
			425					430					435			
AAC	TCC	TGC	AAA	TGC	TGC	ACC	TGG	AAT	TGAGTCGCTA	AAGCCCCTCC						1444
Asn	Ser	Cys	Lys	Cys	Cys	Thr	Trp	Asn								
			440				445									
AGTCCCAGCT	TTGAGGCTGG	GGCCAGGATC	ACTCTACAGC	CTGCCTCCTG	GGTTTCCCT											1504
GGGGGCCGCA	ATCTGGCTCC	TGCAGGCCCTT	TCTGTGGTCT	TCCTTTATCC	AGGCTTTCTG											1564
CTCTCAGCCT	TGCCITCCTT	TTTTCTGGGT	CTCCTGGGCT	GCCCCTTTCA	CTTGCAAAAT											1624
AAATCTTTGG	TTTGTGCCCC	TCAAAAAAAA	AA													1656

(2) INFORMATION FOR SEQ ID NO:4:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 466 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Met	Val	Arg	Ser	Val	Ala	Trp	Ala	Gly	Phe	Met	Val	Leu	Leu	Met	Ile	
-21	-20					-15					-10					
Pro	Trp	Gly	Ser	Ala	Ala	Lys	Leu	Val	Cys	Tyr	Phe	Thr	Asn	Trp	Ala	
-5					1				5					10		
Gln	Tyr	Arg	Gln	Gly	Glu	Ala	Arg	Phe	Leu	Pro	Lys	Asp	Leu	Asp	Pro	

15					20					25					
Ser	Leu	Cys	Thr	His	Leu	Ile	Tyr	Ala	Phe	Ala	Gly	Met	Thr	Asn	His
		30					35					40			
Gln	Leu	Ser	Thr	Thr	Glu	Trp	Asn	Asp	Glu	Thr	Leu	Tyr	Gln	Glu	Phe
	45					50					55				
Asn	Gly	Leu	Lys	Lys	Met	Asn	Pro	Lys	Leu	Lys	Thr	Leu	Leu	Ala	Ile
	60					65					70				75
Gly	Gly	Trp	Asn	Phe	Ser	Thr	Gln	Lys	Phe	Thr	Asp	Met	Val	Ala	Thr
				80					85					90	
Ala	Asn	Asn	Arg	Gln	Thr	Phe	Val	Asn	Ser	Ala	Ile	Arg	Phe	Leu	Arg
			95					100					105		
Lys	Tyr	Ser	Phe	Asp	Gly	Leu	Asp	Leu	Asp	Trp	Glu	Tyr	Pro	Gly	Ser
		110					115					120			
Gln	Gly	Ser	Pro	Ala	Val	Asp	Lys	Glu	Arg	Phe	Thr	Thr	Leu	Val	Gln
	125					130					135				
Asp	Leu	Ala	Asn	Ala	Phe	Gln	Gln	Glu	Ala	Gln	Thr	Ser	Gly	Lys	Glu
	140					145					150				155
Arg	Leu	Leu	Leu	Ser	Ala	Ala	Val	Pro	Ala	Gly	Gln	Thr	Tyr	Val	Asp
				160					165					170	
Ala	Gly	Tyr	Glu	Val	Asp	Lys	Ile	Ala	Gln	Asn	Leu	Asp	Phe	Val	Asn
			175					180					185		
Leu	Met	Ala	Tyr	Asp	Phe	His	Gly	Ser	Trp	Glu	Lys	Val	Thr	Gly	His
		190					195					200			
Asn	Ser	Pro	Leu	Tyr	Lys	Arg	Gln	Glu	Glu	Ser	Gly	Ala	Ala	Ala	Ser
		205				210					215				
Leu	Asn	Val	Asp	Ala	Ala	Val	Gln	Gln	Trp	Leu	Gln	Lys	Gly	Thr	Pro
	220					225					230				235
Ala	Ser	Lys	Leu	Ile	Leu	Gly	Met	Pro	Thr	Tyr	Gly	Arg	Ser	Phe	Thr
			240						245					250	
Leu	Ala	Ser	Ser	Ser	Asp	Thr	Arg	Val	Gly	Ala	Pro	Ala	Thr	Gly	Ser
			255					260					265		
Gly	Thr	Pro	Gly	Pro	Phe	Thr	Lys	Glu	Gly	Gly	Met	Leu	Ala	Tyr	Tyr
		270					275					280			
Glu	Val	Cys	Ser	Trp	Lys	Gly	Ala	Thr	Lys	Gln	Arg	Ile	Gln	Asp	Gln
	285					290					295				
Lys	Val	Pro	Tyr	Ile	Phe	Arg	Asp	Asn	Gln	Trp	Val	Gly	Phe	Asp	Asp
	300					305			310					315	
Val	Glu	Ser	Phe	Lys	Thr	Lys	Val	Ser	Tyr	Leu	Lys	Gln	Lys	Gly	Leu
			320					325					330		
Gly	Gly	Ala	Met	Val	Trp	Ala	Leu	Asp	Leu	Asp	Asp	Phe	Ala	Gly	Phe
			335				340					345			
Ser	Cys	Asn	Gln	Gly	Arg	Tyr	Pro	Leu	Ile	Gln	Thr	Leu	Arg	Gln	Glu
		350					355					360			

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Leu Ser Leu Pro Tyr Leu Pro Ser Gly Thr Pro Glu Leu Glu Val Pro
 365 370 375
 Lys Pro Gly Gln Pro Ser Glu Pro Glu His Gly Pro Ser Pro Gly Gln
 380 385 390 395
 Asp Thr Phe Cys Gln Gly Lys Ala Asp Gly Leu Tyr Pro Asn Pro Arg
 400 405 410
 Glu Arg Ser Ser Phe Tyr Ser Cys Ala Ala Gly Arg Leu Phe Gln Gln
 415 420 425
 Ser Cys Pro Thr Gly Leu Val Phe Ser Asn Ser Cys Lys Cys Cys Thr
 430 435 440
 Trp Asn
 445

(2) INFORMATION FOR SEQ ID NO:5:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 18 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

GACACTATAG AATAGGCC

18

(2) INFORMATION FOR SEQ ID NO:6:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 51 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

TGGGATCATC AGCAGGACCA TGAAACCTGC CCAGGCCACA GACCGCACCA T

51

(2) INFORMATION FOR SEQ ID NO:7:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 40 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

TACATCTAGA ATTATGGCAA AACTGGTCTG CTACTTCACC

40

(2) INFORMATION FOR SEQ ID NO:8:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 34 base pairs
 - (B) TYPE: nucleic acid

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(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

AGATCTAACC TTAGGTGCCT GAAGACAAGT ATGG

34

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 29 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

TACAGAATTC TTATTCACAT CCGGCCCTG

29

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 34 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

TACATCTAGA CTCCATCCAG AAAACAGGT ATGG

34

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 30 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

TCTAGAGTCG ACCTGCAGGC ATGCAAGCTT

30

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

CGCAAGCTTG AGAGCTCCGT TCCGCCACAT GGTGCGGTCT GTGGCCTGGG

50

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(2) INFORMATION FOR SEQ ID NO:13:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 32 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

GACTCTAGAC TAGGTGCCTG AAGGCAAGTA TG

32

(2) INFORMATION FOR SEQ ID NO:14:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 373 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

Ala	Lys	Leu	Val	Cys	Tyr	Phe	Thr	Asn	Trp	Ala	Gln	Tyr	Arg	Gln	Gly	1	5	10	15
Glu	Ala	Arg	Phe	Leu	Pro	Lys	Asp	Leu	Asp	Pro	Ser	Leu	Cys	Thr	His	20	25	30	
Leu	Ile	Tyr	Ala	Phe	Ala	Gly	Met	Thr	Asn	His	Gln	Leu	Ser	Thr	Thr	35	40	45	
Glu	Trp	Asn	Asp	Glu	Thr	Leu	Tyr	Gln	Glu	Phe	Asn	Gly	Leu	Lys	Lys	50	55	60	
Met	Asn	Pro	Lys	Leu	Lys	Thr	Leu	Leu	Ala	Ile	Gly	Gly	Trp	Asn	Phe	65	70	75	80
Gly	Thr	Gln	Lys	Phe	Thr	Asp	Met	Val	Ala	Thr	Ala	Asn	Asn	Arg	Gln	85	90	95	
Thr	Phe	Val	Asn	Ser	Ala	Ile	Arg	Phe	Leu	Arg	Lys	Tyr	Ser	Phe	Asp	100	105	110	
Gly	Leu	Asp	Leu	Asp	Trp	Glu	Tyr	Pro	Gly	Ser	Gln	Gly	Ser	Pro	Ala	115	120	125	
Val	Asp	Lys	Glu	Arg	Phe	Thr	Thr	Leu	Val	Gln	Asp	Leu	Ala	Asn	Ala	130	135	140	
Phe	Gln	Gln	Glu	Ala	Gln	Thr	Ser	Gly	Lys	Glu	Arg	Leu	Leu	Leu	Ser	145	150	155	160
Ala	Ala	Val	Pro	Ala	Gly	Gln	Thr	Tyr	Val	Asp	Ala	Gly	Tyr	Glu	Val	165	170	175	
Asp	Lys	Ile	Ala	Gln	Asn	Leu	Asp	Phe	Val	Asn	Leu	Met	Ala	Tyr	Asp	180	185	190	
Phe	His	Gly	Ser	Trp	Glu	Lys	Val	Thr	Gly	His	Asn	Ser	Pro	Leu	Tyr	195	200	205	

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Lys Arg Gln Glu Glu Ser Gly Ala Ala Ala Ser Leu Asn Val Asp Ala
210 215 220

Ala Val Gln Gln Trp Leu Gln Lys Gly Thr Pro Ala Ser Lys Leu Ile
225 230 235 240

Leu Gly Met Pro Thr Tyr Gly Arg Ser Phe Thr Leu Ala Ser Ser Ser
245 250 255

Asp Thr Arg Val Gly Ala Pro Ala Thr Gly Ser Gly Thr Pro Gly Pro
260 265 270

Phe Thr Lys Glu Gly Gly Met Leu Ala Tyr Tyr Glu Val Cys Ser Trp
275 280 285

Lys Gly Ala Thr Lys Gln Arg Ile Gln Asp Gln Lys Val Pro Tyr Ile
290 295 300

Phe Arg Asp Asn Gln Trp Val Gly Phe Asp Asp Val Glu Ser Phe Lys
305 310 315 320

Thr Lys Val Ser Tyr Leu Lys Gln Lys Gly Leu Gly Gly Ala Met Val
325 330 335

Trp Ala Leu Asp Leu Asp Asp Phe Ala Gly Phe Ser Cys Asn Gln Gly
340 345 350

Arg Tyr Pro Leu Ile Gln Thr Leu Arg Gln Glu Leu Ser Leu Pro Tyr
355 360 365

Leu Pro Ser Gly Thr
370

(2) INFORMATION FOR SEQ ID NO:15:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 373 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

Ala Lys Leu Val Cys Tyr Phe Thr Asn Trp Ala Gln Tyr Arg Gln Gly
1 5 10 15

Glu Ala Arg Phe Leu Pro Lys Asp Leu Asp Pro Ser Leu Cys Thr His
20 25 30

Leu Ile Tyr Ala Phe Ala Gly Met Thr Asn His Gln Leu Ser Thr Thr
35 40 45

Glu Trp Asn Asp Glu Thr Leu Tyr Gln Glu Phe Asn Gly Leu Lys Lys
50 55 60

Met Asn Pro Lys Leu Lys Thr Leu Leu Ala Ile Gly Gly Trp Asn Phe
65 70 75 80

Gly Thr Gln Lys Phe Thr Asp Met Val Ala Thr Ala Asn Asn Arg Gln
85 90 95

Thr Phe Val Asn Ser Ala Ile Arg Phe Leu Arg Lys Tyr Ser Phe Asp
100 105 110

Gly Leu Asp Leu Asp Trp Glu Tyr Pro Gly Ser Gln Gly Ser Pro Ala
115 120 125
Val Asp Lys Glu Arg Phe Thr Thr Leu Val Gln Asp Leu Ala Asn Ala
130 135 140
Phe Gln Gln Glu Ala Gln Thr Ser Gly Lys Glu Arg Leu Leu Leu Ser
145 150 155 160
Ala Ala Val Pro Ala Gly Gln Thr Tyr Val Asp Ala Gly Tyr Glu Val
165 170 175
Asp Lys Ile Ala Gln Asn Leu Asp Phe Val Asn Leu Met Ala Tyr Asp
180 185 190
Phe His Gly Ser Trp Glu Lys Val Thr Gly His Asn Ser Pro Leu Tyr
195 200 205
Lys Arg Gln Glu Glu Ser Gly Ala Ala Ala Ser Leu Asn Val Asp Ala
210 215 220
Ala Val Gln Gln Trp Leu Gln Lys Gly Thr Pro Ala Ser Lys Leu Ile
225 230 235 240
Leu Gly Met Pro Thr Tyr Gly Arg Ser Phe Thr Leu Ala Ser Ser Ser
245 250 255
Asp Thr Arg Val Gly Ala Pro Ala Thr Gly Ser Gly Thr Pro Gly Pro
260 265 270
Phe Thr Lys Glu Gly Gly Met Leu Ala Tyr Tyr Glu Val Cys Ser Trp
275 280 285
Lys Gly Ala Thr Lys Gln Arg Ile Gln Asp Gln Lys Val Pro Tyr Ile
290 295 300
Phe Arg Asp Asn Gln Trp Val Gly Phe Asp Asp Val Glu Ser Phe Lys
305 310 315 320
Thr Lys Val Ser Tyr Leu Lys Gln Lys Gly Leu Gly Gly Ala Met Val
325 330 335
Trp Ala Leu Asp Leu Asp Asp Phe Ala Gly Phe Ser Cys Asn Gln Gly
340 345 350
Arg Tyr Pro Leu Ile Gln Thr Leu Arg Gln Glu Leu Ser Leu Pro Tyr
355 360 365
Leu Ser Ser Gly Thr
370

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